Office Action of April 28, 2008 for record purposes.

DETAILED ACTION

1. The Amendment filed January 11, 2008 in response to the Office Action of October 11, 2007 is acknowledged and has been entered. Previously pending claims 6, 7 and 17 have been cancelled, claims 4, 5, and 8-10 have been amended

2. Claims 4, 5, and 8-10 are currently being examined.

3. The following rejections are being maintained:

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

4. Claims 4, 8, and 9 remain rejected under 35 USC 112, first paragraph for the reasons previously set forth in the Office Action of October 11, 2007, section 12-pages 13-19.

Applicants argue that with respect to the Examiner's assertion that the nucleic acid set forth in SEQ ID NO: 3 can code for a protein or polypeptide that is present in the nucleus of the animal cell, the nucleic acid set forth in SEQ ID NO: 3 can be present both in the nucleus and the cytoplasm.

Applicants argue that in order to assist the Examiner, claim 4, upon which claim 8 also depends, has been amended to define the nucleic acid recited in the claims as the nucleic acid set forth in SEQ ID NO: 3 and a nucleic acid strand that is completely complementary to the nucleic acid set forth in SEQ ID NO: 3. As acknowledged by the Examiner in the Office Action, the present application discloses SEQ ID NO: 3. The present application discloses that the term "nucleic acid of the present invention" can include a complementary strand selected from information of the nucleic acid set forth in SEQ ID NO: 3 (page 22). As is also acknowledged by

the Examiner, it is known in the art that the phrase "complementary strands of nucleic acids" can include nucleic acids that are completely complementary to the claimed polynucleotide.

Applicants arguments have been considered, but have not been found persuasive as the claims are still drawn to fragments of SEQ ID NO: 3. Claims 4, 7 , and 9 are drawn to "A recombinant vector comprising **a purified nucleic acid coding for a** (emphasis added) protein or polypeptide . . . wherein the nucleic acid is set forth **in** (emphasis added) SEQ ID NO: 3 or is a nucleic acid that is completely complementary to the nucleic set forth **in** (emphasis added) SSEQ ID NO: 3. . ." and a host cell transformed with the vector and a method of producing the protein. This claim construction clearly reads on fragments of SEQ ID NO: 3 as the claims are not drawn to the protein or polypeptide produced from a nucleic acid comprising SEQ ID NO: 3. The claims are not enabled to make a fragment of SEQ ID NO: 3 that is present in the nucleus and which has a transcription factor function and/or a function that can induce expression of retinoblastoma gene or a gene product thereof, given that the specification has not identified the regions of the encoded polypeptide that are required for these functions and given the unpredictability of protein biochemistry and predicting function from structure previously set forth. Thus undue experimentation would be required to identify fragments that encode a protein with the claimed functions.

Applicant's arguments have not been found persuasive and the rejection is maintained.

5. Claims 4, 8 and 9 remain rejected under 35 USC 112, first paragraph for the reasons previously set forth in the Office Action of October 11, 2007, section, 13, pages 19-24.

Applicants argue that in order to assist the Examiner, claim 4, upon which claim 8 also depends, has been amended to define the nucleic acid recited in the claims as the nucleic acid set

forth in SEQ ID NO: 3 and a nucleic acid strand that is completely complementary to the nucleic acid set forth in SEQ ID NO: 3. As acknowledged by the Examiner in the Office Action, the present application discloses SEQ ID NO: 3. As is also acknowledged by the Examiner, it is known in the art that the phrase "complementary strands of nucleic acids" can include nucleic acids that are completely complementary to the claimed polynucleotide.

Applicants arguments have been considered, but have not been found persuasive as the claims are still drawn to fragments of SEQ ID NO: 3. Claims 4, 8 , and 9 are drawn to "A recombinant vector comprising **a purified nucleic acid coding for a** (emphasis added) protein or polypeptide . . . wherein the nucleic acid is set forth **in** (emphasis added) SEQ ID NO: 3 or is a nucleic acid that is completely complementary to the nucleic set forth **in** (emphasis added) SSEQ ID NO: 3. . ." and a host cell transformed with the vector and a method of producing the protein. This claim construction clearly reads on fragments of SEQ ID NO: 3 as the claims are not drawn to the protein or polypeptide produced from a nucleic acid comprising SEQ ID NO: 3. Thus, the claims are not enabled to make a fragment of SEQ ID NO: 3 that is present in the nucleus and which has a transcription factor function and/or a function that can induce expression of retinoblastoma gene or a gene product thereof given that the specification has not identify the regions of the encoded polypeptide that are required for these functions and undue experimentation would be required to identify fragments that encode a protein with the claimed functions. The level of skill and knowledge in the art is such that one of ordinary skill would not be able to identify without further testing which of these fragment of SEQ ID NO: 3 can code for a protein have the ability to be present in the nucleus and which has a transcription factor function and/or a function that can induce expression of retinoblastoma gene or a gene product

thereof. Thus one of skill in the art would not recognize that Applicants were in possession of the claimed genus.

Applicant's arguments have not been found persuasive and the rejection is maintained.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

6. Claims 8-10 remain rejected and claims 4 and 5 are rejected under 35 U.S.C. 102(a) as being anticipated by Chano et al. (Oncogene, February 14, 2002, 21:1295-1298, IDS) for the reasons forth in the Office Action of October 11, 2007, section, 15, pages 25-27.

Applicants argue that three of the authors listed in Chano et al., Chano, Ikegawa, and Okabe, are the also the inventors of the present application. The remaining three authors listed in Chano et al., Kontani, Baldini, and Saeki, were working under the direction of the present inventors and their contributions were not of an inventive nature. Applicants submit herewith a Declaration under 37 C.F.R. § 1.132 to further establish that the authors of Chano et al. are the inventors of the present application. As such, Applicants respectfully submit that Chano et al. does not qualify as an invention known or used by "others" within the meaning of 35 U.S.C. §102(a).

The Declaration under 37 CFR 1.132 filed January 11, 2008 is insufficient to overcome the rejection of claims 4, 5 and 8-10 based upon Chano et al. (Oncogene, February 14, 2002, 21:1295-1298, IDS) as set forth in the last Office action because: The Declarants state in section 1:

We, Tokuhiro Chano, Shiro Ikegawa, and Hidetoshi Okabe, do declare and state as follows: **We are three of the six named inventors** (emphasis added) of the present application identified above.

Given the statement that "We are three of the six named inventors" and the identity of the other three inventors has not been made known to the Office nor have six inventors signed the Declaration, the Declaration under 37 CFR 1.132 is not an unequivocal statement from the Applicant regarding the subject matter disclosed in the article and has not properly executed, see MPEP 716.10 and CFR 1.63. Thus, the Declaration under 37 CFR 1.132 filed January 11, 2008 is insufficient to overcome the rejection.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

7. Claim 10 remains rejected under 35 U.S.C. 103(a) as being unpatentable over AB059622 (October 11, 2001), in view of Mensink et al (British J. Haematol. (August 1998) 102:768-774) and further in view of Buck et al (Biotechniques (1999) 27(3):528-536) for the reasons forth in the Office Action of October 11, 2007, section, 16, pages 28-30.

Applicants argue that as acknowledged by the Examiner, AB059622 does not teach the particular primers of SEQ ID Nos: 19 and 20. Mensink et al. and Buck et al. also do not, alone or in combination, teach or suggest SEQ ID Nos: 19 and 20. With reference to the Examiner's

assertion that published sequences may be analyzed by commercially available software for primer selection in many cases, one can use the "Primer 3 website" (primer3.sourceforge.net) for this purpose rather than the commercially available software taught in Mensink et al. Simply by knowing the nucleotide sequence information, one can use the "Primer 3 website" to analyze primer design with general versatility. However, only after using the designed primer, can one obtain useful information on whether or not it is applicable to an experiment or clinical. Thus, one cannot determine if a nucleotide sequence is useful, simply because the sequence is known. Accordingly, one of ordinary skill in the art would not be able to arrive at the particular primers of SEQ ID NOs: 19 and 20, simply because of the disclosure of AB059622.

Applicants arguments have been considered, but have not been found persuasive because of the availability in the art of primer design programs in the art at the time the invention was made and the teaching of Buck that every single primer tested of the 164 primers tested functioned as expected, one of skill in the art would have a reasonable expectation of success given that sequence was known in the art at the time the invention was made.

Applicant's arguments have not been found persuasive and the rejection is maintained.

New Grounds of Rejection

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

8. Claims 4, 5, and 8 are rejected under 35 U.S.C. 102(b) as being anticipated by Nagase et al. (DNA Research, 1996, 3:321-329) as evidenced by Nomura et al. (DNA Research,

1994: 1: 27-35), Chano et al. (Oncogene, February 14, 2002, 21:1295-1298, IDS) and Appendix 1.

The claims are drawn to:

4. A recombinant vector comprising a purified nucleic acid coding for a protein or polypeptide which is present in nucleus of human or animal cell and which has a transcription factor function and/or a function that can induce expression of retinoblastoma gene (RB 1 gene) or a gene product thereof the polypeptide or protein according to claim 1, or a complementary strand thereof, wherein the nucleic acid is set forth in SEQ ID No: 3 or is a nucleic acid strand that is completely complementary to the nucleic acid set forth in SEQ ID No: 3.

5. A recombinant vector comprising a nucleic acid hybridizing under stringent conditions with the a purified nucleic acid set forth in SEQ ID No: 3 or a nucleic acid strand that is completely complementary to the nucleic acid set forth in SEQ ID No: 3 according to claim 3 or the complementary strand thereof; wherein the stringent conditions comprise a condition under which a positive hybridization signal is still observed even after heating at 42 °C in a solution of 6 x SSC, 0.5% SDS and 50% formamide, and washing at 68 °C in a solution of 0.1 x SSC and 0.5% SDS.

8. A transformant that was transformed with the recombinant vector according to claim 4.

Nagase et al. teach the cloning of the cDNA KIAA0203, which 99.3% identical to SEQ ID NO: 3 and codes for a protein identical to RB1CC1, see Table 1 of Nagase et al. and Appendix 1. Nagase et al. used the methods Nomura et al. for cloning the cDNA, see Materials and Methods. and reference 1 of Nagase et al. Nomura et al. teach that cDNA were cloned and

placed into the pBluescript SK+ cDNA vector and used to make cDNA libraries that were grown in colonies of cells, see p. 28, 1st col., of Nomura et al.

Chano et al. teach that RB1CC1 can induce the expression of the RB1 gene, see Abstract, Fig. 2 and Fig.4.

Although the reference does not specifically state that KIAA0203 codes for a protein or polypeptide which is present in nucleus of human or animal cell and which has a transcription factor function and /or a function that can induce expression of retinoblastoma gene (RB1 gene) or a gene product thereof, given the teaching of Chano et al. The claimed product appears to be the same as the prior art product, absent a showing of unobvious differences. The office does not have the facilities and resources to provide the factual evidence needed in order to establish that the product of the prior art does not possess the same material, structural and functional characteristics of the claimed product. In the absence of evidence to the contrary, the burden is on the applicant to prove that the claimed product is different from those taught by the prior art and to establish patentable differences. See In re Best 562F.2d 1252, 195 USPQ 430 (CCPA).

Claim Rejections - 35 USC § 103

The factual inquiries set forth in *Graham* v. *John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

9. Claims 4, 5, 8, and 9 are rejected under 35 U.S.C. 103(a) as being unpatentable over AB059622 (October 11, 2001) as evidenced by Chano et al. (Oncogene, February 14, 2002, 21:1295-1298, IDS), in view of US Patent No. 4,889,806 (Dec. 1989) and Sambrook et al (Molecular Cloning, A Laboratory Manual, Cold Spring Harbor, 1989, pp.16.3-4).

The claims are drawn to:

4. A recombinant vector comprising a purified nucleic acid coding for a protein or polypeptide which is present in nucleus of human or animal cell and which has a transcription factor function and/or a function that can induce expression of retinoblastoma gene (RB 1 gene) or a gene product thereof the polypeptide or protein according to claim 1, or a complementary strand thereof, wherein the nucleic acid is set forth in SEQ ID No: 3 or is a nucleic acid strand that is completely complementary to the nucleic acid set forth in SEQ ID No: 3.

5. A recombinant vector comprising a nucleic acid hybridizing under stringent conditions with the a purified nucleic acid set forth in SEQ ID No: 3 or a nucleic acid strand that is completely complementary to the nucleic acid set forth in SEQ ID No: 3 according to claim 3 or the complementary strand thereof; wherein the stringent conditions comprise a condition

under which a positive hybridization signal is still observed even after heating at 42 °C in a solution of 6 x SSC, 0.5% SDS and 50% formamide, and washing at 68 °C in a solution of 0.1 x SSC and 0.5% SDS.

8. A transformant that was transformed with the recombinant vector according to claim 4.

9. A method for producing a protein or polypeptide which is present in the nucleus of a human or animal cell and which has a transcription factor function and/or a function that can induce expression of retinoblastoma gene (RB 1 gene) or a gene product thereof or a complementary strand thereof, wherein the nucleic acid is set forth in SEQ ID NO" 3 the polypeptide or protein according to claim 1 , comprising a step of culturing the transformant according to claim 8 with the recombinant vector containing nucleic acid coding for the polypeptide or protein.

AB059622 teaches as previously set forth in the Office Action of October 11, 2007, section 14, pages 24-25, but does not teach a recombinant vector comprising SEQ ID NO: 3, a transformant transformed with the recombinant vector, or a method for producing protein using the recombinant vector.

US Patent No. 4,889,806 teach that with the advent of recombinant DNA and molecular cloning technology it is now conventional to transfer genetic information into plasmids or vectors constructed in vitro and then transferred into host cells and clonally propagated (col. 1, lines 18-24).

Sambrook et al teach that cloned genes are conventionally expressed using expression vectors and that expression of cloned proteins have been used to: (1) confirm the identity of a cloned gene by using immunological or functional assays to detect the encoded protein; (2)

produce large amounts of proteins of biological interest that are normally available in only limited quantities from natural sources; (3) to study the biosynthesis and intracellular transport of proteins following their expression in various cell types; and (4) to elucidate structure-function relationships by analyzing the properties of normal and mutant proteins (para bridging pages 16.3 and 16.4).

It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to make a recombinant vector with the nucleic acid sequence of AB059622, transform the vector into a host cell and produce a protein with the methods of Sambrook et al and US Patent No. 4,889,806 because US Patent No. 4,889,806 specifically teaches that it is conventional to transfer genetic materials into plasmids or vectors and then transfer the plasmids or vectors into host cells and clonally propagate the genetic material and because Sambrook et al teach that cloned genes are conventionally expressed using expression vectors.

One of ordinary skill in the art at the time the invention was made would have been motivated to make a recombinant vector with the nucleic acid sequence of AB059622 with the methods of Sambrook et al and US Patent No. 4,889,806 because Sambrook et al specifically teach that expressed cloned proteins are used to: (1) confirm the identity of a cloned gene by using immunological or functional assays to detect the encoded protein; (2) produce large amounts of proteins of biological interest that are normally available in only limited quantities from natural sources; (3) to study the biosynthesis and intracellular transport of proteins following their expression in various cell types; and (4) to elucidate structure-function relationships by analyzing the properties of normal and mutant proteins. Given the conventional nature of the methods, one of skill in the art would have had a reasonable expectation of success.

Priority

10. Applicants state that at page 2, item 6, of the Office Action, the Examiner has acknowledged receipt of papers submitted under 35 U.S.C. §119(a)-(d), which papers have been placed of record in the file. The Examiner recognizes a priority date of January 30, 2003. The Examiner indicates that because the priority of the instantly claimed invention is based on Japanese Application Nos. 2002-161400 and 2002-214978, and translations have not been provided, the Examiner is unable to recognize an earlier priority date. The Examiner suggests that Applicants submit a translation of the priority documents and to point to page and line where support can be found establishing an earlier priority date.

Applicants argue that English translations are not required for claiming priority. According to MPEP § 201.15, the actual merits of an applicant's claim of priority is considered by the Examiner only when a reference is found with an effective date between the date of the foreign filing and the date of filing in the United States. None of the publication dates of the references cited by the Examiner appears to fall within this range. As such, the priority dates of the Japanese applications should be recognized.

Applicants' arguments have been considered and the conditions for foreign priority Japanese Application Nos. 2002-161400 and 2002-214978 have been met.

11. All other objections and rejections recited in Office Action of October 11, 2007 are withdrawn.

12. No claims allowed.

13. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Peter J. Reddig whose telephone number is (571) 272-9031. The examiner can normally be reached on M-F 8:30 a.m.-5:00 p.m.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Larry Helms can be reached on (571) 272-0832. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Peter J Reddig/

Examiner, Art Unit 1642

/P. J. R./

/Karen A Canella/

Primary Examiner, Art Unit 1643

Appendix 1

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D86958
LOCUS       D86958                  6614 bp    mRNA    linear   PRI 15-JAN-2004
DEFINITION  Homo sapiens mRNA for KIAA0203 gene, partial cds.
ACCESSION   D86958
VERSION     D86958.1  GI:1503989
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
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            Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
            Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
  TITLE     Prediction of the coding sequences of unidentified human genes. VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from cell line KG-1 and brain
  JOURNAL   DNA Res. 3 (5), 321-329 (1996)
   PUBMED   9039502
REFERENCE   2  (bases 1 to 6614)
  AUTHORS   Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;
            1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
FEATURES             Location/Qualifiers
     source          1. .6614
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                     /db_xref="taxon:9606"
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                     /cell_line="KG-1"
                     /cell_type="myeloblast"
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                     /gene="KIAA0203"
     5'UTR           1. .515
                     /gene="KIAA0203"
     CDS             <510. .5291
                     /gene="KIAA0203"
                     /note="Start codon is not identified
                     similar to mouse CC1."
                     /citation=[1]
                     /codon_start=1
                     /protein_id="BAA13194.2"
                     /db_xref="GI:40788906"
                     /translation="IIMKLYVFLVNTGTTLTFDTELTVQTVADLKHAIQSKYKIAIQH
                     QVLVVNGGECMAADRRVCTYSAGTDTNPIFLFNKEMILCDRPPAIPKTTFSTENDMEI
                     KVEESLMMPAVFHTVASRTQLALEMYEVAKKLCSFCEGLVHDEHLQHQGWAAIMANLE
                     DCSNSYQKLLFKFESIYSNYLQSIEDIKLKLTHLGTAVSVMAKIPLLECLTRHSYREC
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                     GKEIRESCQSTVHQQDETTIDTKDGDLPFFNVSLLDWINVQDRPNDVESLVRKCFDSM
                     SRLDPRIIRPFIAECRQTIAKLDNQNMKAIKGLEDRLYALDQMIASCGRLVNEQKELA
                     QGFLANQKRAENLKDASVLPDLCLSHANQLMIMLQNHRKLLDIKQKCTTAKQELANNL
                     HVRLKWCCFVMLHADQDGEKLQALLRLVIELLERVKIVEALSTVPQMYCLAVVEVVRR
                     KMFIKHYREWAGALVKDGKRLYEAEKSKRESFGKLFRKSFLRNRLFRGLDSWPPSFCT
                     QKPRKFDCELPDISLKDLQFLQSFCPSEVQPFLRVPLLCDFEPLHQHVLALHNLVKAA
                     QSLDEMSQTITDLLSEQKASVSQTSPQSASSPRMESTAGITTTTSPRTPPPLTVQDPL
                     CPAVCPLEELSPDSIDAHTFDFETIPHPNIEQTIHQVSLDLDSLAESPESDFMSAVNE
                     FVIEENLSSPNPISDPQSPEMMVESLYSSVINAIDSRRMQDTNVCGKEDFGDHTSLNV
                     QLERCRVVAQDSHFSIQTIKEDLCHFRTFVQKEQCDFSNSLKCTAVEIRNIIEKVKCS
                     LEITLKEKHQKELLSLKNEYEGKLDGLIKETEENENKIKKLKGELVCLEEVLQNKDNE
                     FALVKHEKEAVICLQNEKDQKLLEMENIMHSQNCEIKELKQSREIVLEDLKKLHVEND
                     EKLQLLRAELQSLEQSHLKELEDTLQVRHIQEFEKVMTDHRVSLEELKKENQQIINQI
                     QESHAEIIQEKEKQLQELKLKVSDLSDTRCKLEVELALKEAETDEIKILLEESRAQQK
                     ETLKSLLEQETENLRTEISKLNQKIQDNNENYQVGLAELRTLMTIEKDQCISELISRH
                     EEESNILKAELNKVTSLHNQAFEIEKNLKEQIIELQSKLDSELSALERQKDEKITQQE
                     EKYEAIIQNLEKDRQKLVSSQEQDREQLIQKLNCEKDEAIQTALKEFKLEREVVEKEL
                     LEKVKHLENQIAKSPAIDSTRGDSSSLVAELQEKLQEEKAKFLEQLEEQEKRKNEEMQ
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                     RLLEEKKKLEEEVSKLRSSSFVPSPYVATAPELYGACAPELPGESDRSAVETADEGRV
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                     WVLGKVMEKEYCQAKKAQNRFKVPLGTKFYRVKAVSWNKKV"
     3'UTR           5292. .6614
                     /gene="KIAA0203"
ORIGIN
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  Query Match             99.3%;  Score 6587;  DB 5;  Length 6614;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 6609;  Conservative    0;  Mismatches    5;  Indels    9;  Gaps    1;

Qy         10 AACAAACCAAGCCGCGGCGGTGTCCGCGGCCCTGCCGAGCCCTCGGCGTTGCCTCAGAAT 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACAAACCAAGCCGCGGCGGTGTCCGCGGCCCTGCCGAGCCCTCGGCGTTGCCTCAGAAT 60

Qy         70 CCCCCAGTCGCCTGGGCCCCTCGGCTCTGACAGGCCGCGGCCTTCTGTCCCCCGGCCCCA 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCCCAGTCGCCTGGGCCCCTCGGCTCTGACAGGCCGCGGCCTTCTGTCCCCCGGCCCCA 120

Qy        130 GACCCAGAGCCGAGGGGCCTGCTCGCGTCCTTGTCCGCCCCGGACCCCTCCCTGCCTCCTA 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCCAGAGCCGAGGGGCCTGCTCGCGTCCTTGTCCGCCCCGGACCCCTCCCTGCCTCCTA 180

Qy        190 GAGTTCGGGGCCGCGGCGGGCGGGCGCCCGGGACGCCGGCGGTTGTGTCGGCTTAGCGGT 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGTTCGGGGCCGCGGCGGGCGGGCGCCCGGGACGCCGGCGGTTGTGTCGGCTTAGCGGT 240

Qy        250 GCCGAATGGGCGGTTGGTAACCGCTGCCGAGGACTAGGCGGCGGCGGAAGATGGTGCCGG 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAATGGGCGGTTGGTAACCGCTGCCGAGGACTAGGCGGCGGCGGAAGATGGTGCCGG 300

Qy        310 GGGTCGCTGGCTCTGCTGCTGCCGCCGGCGAAGGAGGAGGCGTTGCCGGTTTTCTGAGTT 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGTCGCTGGCTCTGCTGCTGCCGCCGGCGAAGGAGGAGGCGTTGCCGGTTTTCTGAGTT 360

Qy        370 TAACCAGTAATGCCATTCAGTTGCCAATCTCAAGCAAAGCAAACATAAGCCAGTTTTAAT 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACCAGTAATGCCATTCAGTTGCCAATCTCAAGCAAAGCAAACATAAGCCAGTTTTAAT 420

Qy        430 CTACTTTTTAAGAAAAGTGGTAGTCCTTTTCACAGTGCCTGACGTAACTGTATCAGAGGG 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTACTTTTTAAGAAAAGTGGTAGTCCTTTTCACAGTGCCTGACGTAACTGTATCAGAGGG 480

Qy        490 TGAGGTATAAGCTCACAGAATTCAGATAAATCATCATGAAGTTATATGTATTTCTGGTTA 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGAGGTATAAGCTCACAGAATTCAGATAAATCATCATGAAGTTATATGTATTTCTGGTTA 540

Qy        550 ACACTGGAACTACTCTAACATTTGACACTGAACTTACAGTGCAAACTGTGGCAGACCTTA 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACACTGGAACTACTCTAACATTTGACACTGAACTTACAGTGCAAACTGTGGCAGACCTTA 600

Qy        610 AGCATGCCATTCAAAGCAAATACAAGATTGCTATTCAACACCAGGTGCTGGTGGTCAATG 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCATGCCATTCAAAGCAAATACAAGATTGCTATTCAACACCAGGTGCTGGTGGTCAATG 660

Qy        670 GAGGAGAATGCATGGCTGCAGATCGAAGAGTGTGTACCTACAGTGCTGGGACGGATACAA 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGGAGAATGCATGGCTGCAGATCGAAGAGTGTGTACCTACAGTGCTGGGACGGATACAA 720

Qy        730 ATCCAATTTTTCTTTTTAACAAAGAAATGATCTTATGCGATCGTCCACCTGCTATTCCTA 789
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        721 ATCCAATTTTTCTTTTTAACAAAGAAATGATCTTATGTGATCGTCCACCTGCTATTCCTA 780

Qy        790 AAACTACCTTTTCGACAGAAAATGACATGGAAATAAAAGTTGAAGAATCTCTTATGATGC 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAACTACCTTTTCGACAGAAAATGACATGGAAATAAAAGTTGAAGAATCTCTTATGATGC 840

Qy        850 CTGCAGTTTTTCATACTGTTGCTTCAAGGACACAGCTTGCATTGGAAATGTATGAAGTTG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTGCAGTTTTTCATACTGTTGCTTCAAGGACACAGCTTGCATTGGAAATGTATGAAGTTG 900

Qy        910 CCAAGAAACTTTGTTCTTTTTGTGAAGGTCTTGTACATGATGAACATCTTCAACACCAAG 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          901 CCAAGAAACTTTGTTCTTTTTGTGAAGGTCTTGTACATGATGAACATCTTCAACACCAAG 960

Qy          970 GCTGGGCTGCAATCATGGCCAACCTGGAGGACTGTTCAAATTCATACCAAAAGCTACTTT 1029
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 GCTGGGCTGCAATCATGGCCAACCTGGAGGACTGTTCAAATTCATACCAAAAGCTACTTT 1020

Qy         1030 TCAAGTTTGAAAGTATTTATTCAAATTATCTGCAGTCCATAGAAGACATCAAGTTAAAAC 1089
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 TCAAGTTTGAAAGTATTTATTCAAATTATCTGCAGTCCATAGAAGACATCAAGTTAAAAC 1080

Qy         1090 TTACTCATTTAGGAACTGCAGTTTCAGTAATGGCCAAGATTCCACTGTTGGAGTGCCTAA 1149
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 TTACTCATTTAGGAACTGCAGTTTCAGTAATGGCCAAGATTCCACTGTTGGAGTGCCTAA 1140

Qy         1150 CCAGACATAGTTACAGAGAATGTTTGGGAAGACTGGATTCTTTACCTGAACATGAAGACT 1209
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 CCAGACATAGTTACAGAGAATGTTTGGGAAGACTGGATTCTTTACCTGAACATGAAGACT 1200

Qy         1210 CAGAAAAAGCTGAGACGAAAAGATCCACTGAACTGGTGCTCTCTCCTGATATGCCTAGAA 1269
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 CAGAAAAAGCTGAGACGAAAAGATCCACTGAACTGGTGCTCTCTCCTGATATGCCTAGAA 1260

Qy         1270 CAACTAACGAATCTTTGTTAACCTCATTTCCCAAGTCAGTGGAACATGTGTCCCCAGATA 1329
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 CAACTAACGAATCTTTGTTAACCTCATTTCCCAAGTCAGTGGAACATGTGTCCCCAGATA 1320

Qy         1330 CCGCAGATGCTGAAAGTGGCAAAGAAATTAGGGAATCTTGTCAAAGTACTGTTCATCAGC 1389
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 CCGCAGATGCTGAAAGTGGCAAAGAAATTAGGGAATCTTGTCAAAGTACTGTTCATCAGC 1380

Qy         1390 AAGATGAAACTACGATTGACACTAAAGATGGTGATCTGCCCTTTTTTAATGTCTCTTTGT 1449
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1381 AAGATGAAACTACGATTGACACTAAAGATGGTGATCTGCCCTTTTTTAATGTCTCTTTGT 1440

Qy         1450 TAGACTGGATAAATGTTCAAGATAGACCTAATGATGTGGAATCTTTGGTCAGGAAGTGCT 1509
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1441 TAGACTGGATAAATGTTCAAGATAGACCTAATGATGTGGAATCTTTGGTCAGGAAGTGCT 1500

Qy         1510 TTGATTCTATGAGCAGGCTTGATCCAAGGATTATTCGACCATTTATAGCAGAATGCCGTC 1569
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1501 TTGATTCTATGAGCAGGCTTGATCCAAGGATTATTCGACCATTTATAGCAGAATGCCGTC 1560

Qy         1570 AAACTATTGCCAAACTTGATAATCAGAATATGAAAGCCATTAAAGGACTTGAAGATCGGC 1629
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1561 AAACTATTGCCAAACTTGATAATCAGAATATGAAAGCCATTAAAGGACTTGAAGATCGGC 1620

Qy         1630 TCTACGCCCTGGACCAGATGATTGCTAGCTGTGGCCGACTGGTGAATGAACAGAAAGAGC 1689
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1621 TCTACGCCCTGGACCAGATGATTGCTAGCTGTGGCCGACTGGTGAATGAACAGAAAGAGC 1680

Qy         1690 TTGCTCAGGGATTTTTAGCTAATCAGAAGAGAGCTGAAAACTTAAAGGATGCATCTGTAT 1749
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1681 TTGCTCAGGGATTTTTAGCTAATCAGAAGAGAGCTGAAAACTTAAAGGATGCATCTGTAT 1740

Qy         1750 TACCTGATTTATGCCTGAGTCACGCAAATCAGTTGATGATTATGTTGCAAAATCATAGAA 1809
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1741 TACCTGATTTATGCCTGAGTCACGCAAATCAGTTGATGATTATGTTGCAAAATCATAGAA 1800

Qy         1810 AACTGTTAGATATTAAGCAGAAGTGTACCACTGCCAAACAAGAACTAGCAAATAACCTAC 1869
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1801 AACTGTTAGATATTAAGCAGAAGTGTACCACTGCCAAACAAGAACTAGCAAATAACCTAC 1860

Qy         1870 ATGTCAGACTGAAGTGGTGTTGCTTTGTAATGCTTCATGCTGATCAAGATGGAGAGAAGT 1929
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1861 ATGTCAGACTGAAGTGGTGTTGCTTTGTAATGCTTCATGCTGATCAAGATGGAGAGAAGT 1920

Qy         1930 TACAAGCTTTGCTCCGCCTCGTAATAGAGCTGTTAGAAAGAGTCAAAATTGTTGAAGCTC 1989
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TACAAGCTTTGCTCCGCCTCGTAATAGAGCTGTTAGAAAGAGTCAAAATTGTTGAAGCTC 1980

Qy       1990 TTAGTACAGTTCCTCAGATGTACTGCTTAGCTGTTGTTGAGGTTGTAAGAAGAAAAATGT 2049
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TTAGTACAGTTCCTCAGATGTACTGCTTAGCTGTTGTTGAGGTTGTAAGAAGAAAAATGT 2040

Qy       2050 TCATAAAACACTACAGGGAGTGGGCTGGTGCTTTAGTCAAAGATGGAAAGAGATTATATG 2109
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TCATAAAACACTACAGGGAGTGGGCTGGTGCTTTAGTCAAAGATGGAAAGAGATTATATG 2100

Qy       2110 AAGCAGAAAAATCAAAAAGGGAATCCTTTGGGAAATTATTTAGGAAGTCTTTTTTAAGAA 2169
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AAGCAGAAAAATCAAAAAGGGAATCCTTTGGGAAATTATTTAGGAAGTCTTTTTTAAGAA 2160

Qy       2170 ATCGTCTGTTTAGGGGACTGGACTCCTGGCCCCCTTCCTTTTGTACTCAAAAGCCTCGAA 2229
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 ATCGTCTGTTTAGGGGACTGGACTCCTGGCCCCCTTCCTTTTGTACTCAAAAGCCTCGAA 2220

Qy       2230 AGTTTGACTGTGAACTTCCAGATATTTCATTAAAAGATTTACAGTTTCTGCAATCATTTT 2289
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AGTTTGACTGTGAACTTCCAGATATTTCATTAAAAGATTTACAGTTTCTGCAATCATTTT 2280

Qy       2290 GTCCTTCGGAAGTTCAGCCATTCCTCAGGGTTCCCTTACTTTGTGACTTTGAACCTCTAC 2349
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GTCCTTCGGAAGTTCAGCCATTCCTCAGGGTTCCCTTACTTTGTGACTTTGAACCTCTAC 2340

Qy       2350 ACCAGCATGTACTTGCTCTACATAATTTGGTAAAAGCAGCACAAAGTTTGGATGAAATGT 2409
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 ACCAGCATGTACTTGCTCTACATAATTTGGTAAAAGCAGCACAAAGTTTGGATGAAATGT 2400

Qy       2410 CACAGACCATTACAGATCTACTGAGTGAACAAAAGGCATCTGTGAGCCAGACATCCCCAC 2469
                |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db       2401 CACAGACCATTACAGATCTACTGAGTGAACAAAAGGCATCTGTGAGTCAGACATCCCCAC 2460

Qy       2470 AGTCTGCTTCTTCACCAAGGATGGAAAGTACAGCAGGAATTACAACTACTACCTCACCGA 2529
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 AGTCTGCTTCTTCACCAAGGATGGAAAGTACAGCAGGAATTACAACTACTACCTCACCGA 2520

Qy       2530 GAACTCCTCCACCACTGACTGTTCAGGATCCCTTATGTCCTGCAGTTTGTCCCTTAGAAG 2589
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GAACTCCTCCACCACTGACTGTTCAGGATCCCTTATGTCCTGCAGTTTGTCCCTTAGAAG 2580

Qy       2590 AATTATCTCCAGATAGTATTGATGCACATACGTTTGATTTTGAAACTATTCCCCATCCAA 2649
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AATTATCTCCAGATAGTATTGATGCACATACGTTTGATTTTGAAACTATTCCCCATCCAA 2640

Qy       2650 ACATAGAACAGACTATTCACCAAGTTTCTTTAGACTTGGATTCATTAGCAGAAAGTCCTG 2709
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 ACATAGAACAGACTATTCACCAAGTTTCTTTAGACTTGGATTCATTAGCAGAAAGTCCTG 2700

Qy       2710 AATCAGATTTTATGTCTGCTGTGAATGAGTTTGTAATAGAAGAAAATTTGTCGTCTCCTA 2769
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 AATCAGATTTTATGTCTGCTGTGAATGAGTTTGTAATAGAAGAAAATTTGTCGTCTCCTA 2760

Qy       2770 ATCCTATAAGTGATCCACAAAGCCCAGAAATGATGGTGGAATCACTTTATTCATCAGTTA 2829
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 ATCCTATAAGTGATCCACAAAGCCCAGAAATGATGGTGGAATCACTTTATTCATCAGTTA 2820

Qy       2830 TCAATGCGATAGACAGTAGACGAATGCAGGATACAAATGTATGTGGTAAGGAGGATTTTG 2889
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 TCAATGCGATAGACAGTAGACGAATGCAGGATACAAATGTATGTGGTAAGGAGGATTTTG 2880

Qy       2890 GAGATCATACTTCTCTGAATGTCCAGTTGGAAAGATGTAGAGTTGTTGCCCAAGACTCTC 2949
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GAGATCATACTTCTCTGAATGTCCAGTTGGAAAGATGTAGAGTTGTTGCCCAAGACTCTC 2940
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Qy        2950 ACTTCAGTATACAAACCATTAAGGAAGACCTTTGCCACTTTAGAACATTTGTACAAAAAG 3009
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2941 ACTTCAGTATACAAACCATTAAGGAAGACCTTTGCCACTTTAGAACATTTGTACAAAAAG 3000

Qy        3010 AACAGTGTGACTTCTCAAATTCATTAAAATGTACAGCAGTAGAAATAAGAAACATTATTG 3069
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3001 AACAGTGTGACTTCTCAAATTCATTAAAATGTACAGCAGTAGAAATAAGAAACATTATTG 3060

Qy        3070 AAAAAGTAAAATGTTCTCTGGAAATAACACTAAAAGAAAAACATCAAAAAGAACTACTGT 3129
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3061 AAAAAGTAAAATGTTCTCTGGAAATAACACTAAAAGAAAAACATCAAAAAGAACTACTGT 3120

Qy        3130 CTTTAAAAAATGAATATGAAGGTAAACTTGACGGACTAATAAAGGAAACTGAAGAGAATG 3189
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3121 CTTTAAAAAATGAATATGAAGGTAAACTTGACGGACTAATAAAGGAAACTGAAGAGAATG 3180

Qy        3190 AAAACAAAATTAAAAAATTGAAGGGAGAGTTAGTATGCCTTGAGGAGGTTTTACAAAATA 3249
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3181 AAAACAAAATTAAAAAATTGAAGGGAGAGTTAGTATGCCTTGAGGAGGTTTTACAAAATA 3240

Qy        3250 AAGATAATGAATTTGCTTTGGTTAAACATGAAAAAGAAGCTGTAATCTGCCTGCAGAATG 3309
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3241 AAGATAATGAATTTGCTTTGGTTAAACATGAAAAAGAAGCTGTAATCTGCCTGCAGAATG 3300

Qy        3310 AAAAGGATCAGAAGTTGTTAGAGATGGAAAATATAATGCACTCTCAAAATTGTGAAATTA 3369
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3301 AAAAGGATCAGAAGTTGTTAGAGATGGAAAATATAATGCACTCTCAAAATTGTGAAATTA 3360

Qy        3370 AAGAACTGAAGCAGTCACGAGAAATAGTGTTAGAAGACTTAAAAAAGCTCCATGTTGAAA 3429
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3361 AAGAACTGAAGCAGTCACGAGAAATAGTGTTAGAAGACTTAAAAAAGCTCCATGTTGAAA 3420

Qy        3430 ATGATGAGAAGTTACAGTTATTGAGGGCAGAACTTCAGTCCTTGGAGCAAAGTCATCTAA 3489
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3421 ATGATGAGAAGTTACAGTTATTGAGGGCAGAACTTCAGTCCTTGGAGCAAAGTCATCTAA 3480

Qy        3490 AGGAATTAGAGGACACACTTCAGGTTAGGCACATACAAGAGTTTGAGAAGGTTATGACAG 3549
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3481 AGGAATTAGAGGACACACTTCAGGTTAGGCACATACAAGAGTTTGAGAAGGTTATGACAG 3540

Qy        3550 ACCACAGAGTTTCTTTGGAGGAATTAAAAAAGGAAAATCAACAAATAATTAATCAAATAC 3609
               ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        3541 ACCACAGAGTTTCTTTGGAGGAATTAAAAAAGGAAAACCAACAAATAATTAATCAAATAC 3600

Qy        3610 AAGAATCTCATGCTGAAATTATCCAGGAAAAAGAAAAACAGTTACAGGAATTAAAACTCA 3669
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3601 AAGAATCTCATGCTGAAATTATCCAGGAAAAAGAAAAACAGTTACAGGAATTAAAACTCA 3660

Qy        3670 AGGTTTCTGATTTGTCAGACACGAGATGCAAGTTAGAGGTTGAACTTGCGTTGAAGGAAG 3729
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3661 AGGTTTCTGATTTGTCAGACACGAGATGCAAGTTAGAGGTTGAACTTGCGTTGAAGGAAG 3720

Qy        3730 CAGAAACTGATGAAATAAAAATTTTGCTGGAAGAAAGCAGAGCCCAGCAGAAGGAGACCT 3789
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3721 CAGAAACTGATGAAATAAAAATTTTGCTGGAAGAAAGCAGAGCCCAGCAGAAGGAGACCT 3780

Qy        3790 TGAAATCTCTTCTTGAACAAGAGACAGAAAATTTGAGAACAGAAATTAGTAAACTCAACC 3849
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3781 TGAAATCTCTTCTTGAACAAGAGACAGAAAATTTGAGAACAGAAATTAGTAAACTCAACC 3840

Qy        3850 AAAAGATTCAGGATAATAATGAAAATTATCAGGTGGGCTTAGCAGAGCTAAGAACTTTAA 3909
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3841 AAAAGATTCAGGATAATAATGAAAATTATCAGGTGGGCTTAGCAGAGCTAAGAACTTTAA 3900

Qy        3910 TGACAATTGAAAAAGATCAGCGTATTTCCGAGTTAATTAGTAGACATGAAGAAGAATCTA 3969
               |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        3901 TGACAATTGAAAAAGATCAGTGTATTTCCGAGTTAATTAGTAGACATGAAGAAGAATCTA 3960
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Qy        3970 ATATACTTAAAGCTGAATTAAACAAAGTAACATCTTTGCATAACCAAGCATTTGAAATAG 4029
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3961 ATATACTTAAAGCTGAATTAAACAAAGTAACATCTTTGCATAACCAAGCATTTGAAATAG 4020

Qy        4030 AAAAAAACCTAAAAGAACAAATAATTGAACTGCAGAGTAAATTGGATTCAGAATTGAGTG 4089
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4021 AAAAAAACCTAAAAGAACAAATAATTGAACTGCAGAGTAAATTGGATTCAGAATTGAGTG 4080

Qy        4090 CTCTTGAAAGACAAAAAGATGAAAAAATTACCCAACAAGAAGAGAAATACGAAGCTATTA 4149
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4081 CTCTTGAAAGACAAAAAGATGAAAAAATTACCCAACAAGAAGAGAAATACGAAGCTATTA 4140

Qy        4150 TCCAGAACCTTGAGAAAGACAGACAAAAATTGGTCAGCAGCCAGGAGCAAGACAGAGAAC 4209
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4141 TCCAGAACCTTGAGAAAGACAGACAAAAATTGGTCAGCAGCCAGGAGCAAGACAGAGAAC 4200

Qy        4210 AGTTAATTCAGAAGCTTAATTGTGAAAAAGATGAAGCTATTCAGACTGCCCTAAAAGAAT 4269
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4201 AGTTAATTCAGAAGCTTAATTGTGAAAAAGATGAAGCTATTCAGACTGCCCTAAAAGAAT 4260

Qy        4270 TTAAATTGGAGAGAGAAGTTGTTGAGAAAGAGTTATTAGAAAAAGTTAAACATCTTGAGA 4329
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4261 TTAAATTGGAGAGAGAAGTTGTTGAGAAAGAGTTATTAGAAAAAGTTAAACATCTTGAGA 4320

Qy        4330 ATCAAATAGCAAAAAGTCCTGCCATTGACTCTACCAGAGGAGATTCTTCAAGCTTAGTTG 4389
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4321 ATCAAATAGCAAAAAGTCCTGCCATTGACTCTACCAGAGGAGATTCTTCAAGCTTAGTTG 4380

Qy        4390 CTGAACTTCAAGAAAAGCTTCAGGAAGAAAAAGCTAAGTTTCTAGAACAACTTGAAGAGC 4449
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4381 CTGAACTTCAAGAAAAGCTTCAGGAAGAAAAAGCTAAGTTTCTAGAACAACTTGAAGAGC 4440

Qy        4450 AAGAAAAAAGAAAGAATGAAGAAATGCAAAATGTTCGAACATCTTTGATTGCGGAACAAC 4509
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4441 AAGAAAAAAGAAAGAATGAAGAAATGCAAAATGTTCGAACATCTTTGATTGCGGAACAAC 4500

Qy        4510 AGACCAATTTTAACACTGTTTTAACAAGAGAGAAAATGAGAAAAGAAAACATAATAAATG 4569
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4501 AGACCAATTTTAACACTGTTTTAACAAGAGAGAAAATGAGAAAAGAAAACATAATAAATG 4560

Qy        4570 ATCTTAGTGATAAGTTGAAAAGTACAATGCAGCAACAAGAACGGGATAAAGATTTGATAG 4629
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4561 ATCTTAGTGATAAGTTGAAAAGTACAATGCAGCAACAAGAACGGGATAAAGATTTGATAG 4620

Qy        4630 AGTCACTTTCTGAAGATCGAGCTCGTTTGCTTGAGGAAAAGAAAAAGCTTGAAGAAGAAG 4689
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4621 AGTCACTTTCTGAAGATCGAGCTCGTTTGCTTGAGGAAAAGAAAAAGCTTGAAGAAGAAG 4680

Qy        4690 TCAGTAAGTTGCGCAGTAGCAGTTTTGTTCCTTCACCATATGTAGCTACAGCCCCAGAAC 4749
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4681 TCAGTAAGTTGCGCAGTAGCAGTTTTGTTCCTTCACCATATGTAGCTACAGCCCCAGAAC 4740

Qy        4750 TTTATGGAGCTTGTGCACCTGAACTCCCAGGTGAATCAGATAGATCCGCTGTGGAAACAG 4809
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4741 TTTATGGAGCTTGTGCACCTGAACTCCCAGGTGAATCAGATAGATCCGCTGTGGAAACAG 4800

Qy        4810 CAGATGAAGGAAGAGTGGATTCAGCAATGGAGACAAGCATGATGTCTGTACAAGAAAATA 4869
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4801 CAGATGAAGGAAGAGTGGATTCAGCAATGGAGACAAGCATGATGTCTGTACAAGAAAATA 4860

Qy        4870 TTCATATGTTGTCTGAAGAAAAACAGCGGATAATGCTGTTAGAACGAACATTGCAATTGA 4929
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4861 TTCATATGTTGTCTGAAGAAAAACAGCGGATAATGCTGTTAGAACGAACATTGCAATTGA 4920

Qy        4930 AAGAAGAAGAAAATAAACGGTTAAATCAAAGACTGATGTCTCAGAGCATGTCTTCAGTAT 4989
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        4921 AAGAAGAAGAAAATAAACGGTTAAATCAAAGACTGATGTCTCAGAGCATGTCTTCAGTAT 4980

Qy        4990 CTTCAAGGCATTCTGAAAAGATAGCTATTAGAGATTTTCAGGTGGGAGATTTGGTACTCA 5049
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4981 CTTCAAGGCATTCTGAAAAGATAGCTATTAGAGATTTTCAGGTGGGAGATTTGGTACTCA 5040

Qy        5050 TCATCCTAGACGAACGCCATGACAATTATGTGTTATTTACTGTTAGTCCTACTTTATATT 5109
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5041 TCATCCTAGACGAACGCCATGACAATTATGTGTTATTTACTGTTAGTCCTACTTTATATT 5100

Qy        5110 TTCTACATTCAGAGTCTCTACCTGCCCTGGATCTCAAACCAGGTGAGGGTGCTTCAGGTG 5169
               |||||||||||||||||||||||||||||||||||||||||         ||||||||||
Db        5101 TTCTACATTCAGAGTCTCTACCTGCCCTGGATCTCAAACCA---------GCTTCAGGTG 5151

Qy        5170 CATCTAGAAGACCCTGGGTACTTGGAAAAGTAATGGAAAAAGAATACTGTCAAGCCAAAA 5229
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VERSION     D86958  GI:1503989
KEYWORDS    KIAA0203 protein.
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 6614)
  AUTHORS   Nomura,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1996) Nobuo Nomura, Kazusa DNA Research
            Institute; 1532-3 Yanauchino, Kisarazu, Chiba 292, Japan
            (E-mail:cdnainfo@kazusa.or.jp, Tel:0483-52-3930, Fax:0483-52-3931)
REFERENCE   2  (bases 1 to 6614)
  AUTHORS   Nagase,T., Seki,N., Ishikawa,K., Ohara,O. and Nomura,N.
  TITLE     Prediction of the coding sequences of unidentified human genes. VI.
            The coding sequences of 80 new genes (KIAA 0201 - KIAA 0280)
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            deduced by analysis of cDNA clones from human cell line KG-1 and
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  JOURNAL   Unpublished (1996)
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     6541 caaaatggaa taaacatcat agtgtataga aaactgaatt tgacaagtta atgaataaat
     6601 gaacaaatga tttc
//
```

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

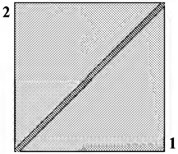
Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 0 expect: 300.0 wordsize: 3 Filter View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: gi|40788906|KIAA0203 [Homo sapiens]
Length = 1593 (1 .. 1593)

Sequence 2: gi|119607126|RB1-inducible coiled-coil 1, isoform CRA_b [Homo sapiens]
>gi|168272926|dbj|BAG10302.1| RB1-inducible coiled-coil protein 1 [synthetic construct]

Length = 1591 (1 .. 1591)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 3112 bits (8067),  Expect = 0.0
 Identities = 1591/1591 (100%), Positives = 1591/1591 (100%), Gaps = 0/1591 (0%)

Query  3     MKLYVFLVNTGTTLTFDTELTVQTVADLKHAIQSKYKIAIQHQVLVVNGGECMAADRRVC  62
             MKLYVFLVNTGTTLTFDTELTVQTVADLKHAIQSKYKIAIQHQVLVVNGGECMAADRRVC
Sbjct  1     MKLYVFLVNTGTTLTFDTELTVQTVADLKHAIQSKYKIAIQHQVLVVNGGECMAADRRVC  60

Query  63    TYSAGTDTNPIFLFNKEMILCDRPPAIPKTTFSTENDMEIKVEESLMMPAVFHTVASRTQ  122
             TYSAGTDTNPIFLFNKEMILCDRPPAIPKTTFSTENDMEIKVEESLMMPAVFHTVASRTQ
Sbjct  61    TYSAGTDTNPIFLFNKEMILCDRPPAIPKTTFSTENDMEIKVEESLMMPAVFHTVASRTQ  120

Query  123   LALEMYEVAKKLCSFCEGLVHDEHLQHQGWAAIMANLEDCSNSYQKLLFKFESIYSNYLQ  182
             LALEMYEVAKKLCSFCEGLVHDEHLQHQGWAAIMANLEDCSNSYQKLLFKFESIYSNYLQ
Sbjct  121   LALEMYEVAKKLCSFCEGLVHDEHLQHQGWAAIMANLEDCSNSYQKLLFKFESIYSNYLQ  180

Query  183   SIEDIKLKLTHLGTAVSVMAKIPLLECLTRHSYRECLGRLDSLPEHEDSEKAETKRSTEL  242
             SIEDIKLKLTHLGTAVSVMAKIPLLECLTRHSYRECLGRLDSLPEHEDSEKAETKRSTEL
Sbjct  181   SIEDIKLKLTHLGTAVSVMAKIPLLECLTRHSYRECLGRLDSLPEHEDSEKAETKRSTEL  240

Query  243   VLSPDMPRTTNESLLTSFPKSVEHVSPDTADAESGKEIRESCQSTVHQQDETTIDTKDGD  302
             VLSPDMPRTTNESLLTSFPKSVEHVSPDTADAESGKEIRESCQSTVHQQDETTIDTKDGD
Sbjct  241   VLSPDMPRTTNESLLTSFPKSVEHVSPDTADAESGKEIRESCQSTVHQQDETTIDTKDGD  300

Query  303   LPFFNVSLLDWINVQDRPNDVESLVRKCFDSMSRLDPRIIRPFIAECRQTIAKLDNQNMK  362
             LPFFNVSLLDWINVQDRPNDVESLVRKCFDSMSRLDPRIIRPFIAECRQTIAKLDNQNMK
Sbjct  301   LPFFNVSLLDWINVQDRPNDVESLVRKCFDSMSRLDPRIIRPFIAECRQTIAKLDNQNMK  360

Query  363   AIKGLEDRLYALDQMIASCGRLVNEQKELAQGFLANQKRAENLKDASVLPDLCLSHANQL  422
             AIKGLEDRLYALDQMIASCGRLVNEQKELAQGFLANQKRAENLKDASVLPDLCLSHANQL
Sbjct  361   AIKGLEDRLYALDQMIASCGRLVNEQKELAQGFLANQKRAENLKDASVLPDLCLSHANQL  420

Query  423   MIMLQNHRKLLDIKQKCTTAKQELANNLHVRLKWCCFVMLHADQDGEKLQALLRLVIELL  482
             MIMLQNHRKLLDIKQKCTTAKQELANNLHVRLKWCCFVMLHADQDGEKLQALLRLVIELL
Sbjct  421   MIMLQNHRKLLDIKQKCTTAKQELANNLHVRLKWCCFVMLHADQDGEKLQALLRLVIELL  480

Query  483   ERVKIVEALSTVPQMYCLAVVEVVRRKMFIKHYREWAGALVKDGKRLYEAEKSKRESFGK  542
             ERVKIVEALSTVPQMYCLAVVEVVRRKMFIKHYREWAGALVKDGKRLYEAEKSKRESFGK
Sbjct  481   ERVKIVEALSTVPQMYCLAVVEVVRRKMFIKHYREWAGALVKDGKRLYEAEKSKRESFGK  540

Query  543   LFRKSFLRNRLFRGLDSWPPSFCTQKPRKFDCELPDISLKDLQFLQSFCPSEVQPFLRVP  602
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            LFRKSFLRNRLFRGLDSWPPSFCTQKPRKFDCELPDISLKDLQFLQSFCPSEVQPFLRVP
Sbjct  541  LFRKSFLRNRLFRGLDSWPPSFCTQKPRKFDCELPDISLKDLQFLQSFCPSEVQPFLRVP  600

Query  603  LLCDFEPLHQHVLALHNLVKAAQSLDEMSQTITDLLSEQKASVSQTSPQSASSPRMESTA  662
            LLCDFEPLHQHVLALHNLVKAAQSLDEMSQTITDLLSEQKASVSQTSPQSASSPRMESTA
Sbjct  601  LLCDFEPLHQHVLALHNLVKAAQSLDEMSQTITDLLSEQKASVSQTSPQSASSPRMESTA  660

Query  663  GITTTTSPRTPPPLTVQDPLCPAVCPLEELSPDSIDAHTFDFETIPHPNIEQTIHQVSLD  722
            GITTTTSPRTPPPLTVQDPLCPAVCPLEELSPDSIDAHTFDFETIPHPNIEQTIHQVSLD
Sbjct  661  GITTTTSPRTPPPLTVQDPLCPAVCPLEELSPDSIDAHTFDFETIPHPNIEQTIHQVSLD  720

Query  723  LDSLAESPESDFMSAVNEFVIEENLSSPNPISDPQSPEMMVESLYSSVINAIDSRRMQDT  782
            LDSLAESPESDFMSAVNEFVIEENLSSPNPISDPQSPEMMVESLYSSVINAIDSRRMQDT
Sbjct  721  LDSLAESPESDFMSAVNEFVIEENLSSPNPISDPQSPEMMVESLYSSVINAIDSRRMQDT  780

Query  783  NVCGKEDFGDHTSLNVQLERCRVVAQDSHFSIQTIKEDLCHFRTFVQKEQCDFSNSLKCT  842
            NVCGKEDFGDHTSLNVQLERCRVVAQDSHFSIQTIKEDLCHFRTFVQKEQCDFSNSLKCT
Sbjct  781  NVCGKEDFGDHTSLNVQLERCRVVAQDSHFSIQTIKEDLCHFRTFVQKEQCDFSNSLKCT  840

Query  843  AVEIRNIIEKVKCSLEITLKEKHQKELLSLKNEYEGKLDGLIKETEENENKIKKLKGELV  902
            AVEIRNIIEKVKCSLEITLKEKHQKELLSLKNEYEGKLDGLIKETEENENKIKKLKGELV
Sbjct  841  AVEIRNIIEKVKCSLEITLKEKHQKELLSLKNEYEGKLDGLIKETEENENKIKKLKGELV  900

Query  903  CLEEVLQNKDNEFALVKHEKEAVICLQNEKDQKLLEMENIMHSQNCEIKELKQSREIVLE  962
            CLEEVLQNKDNEFALVKHEKEAVICLQNEKDQKLLEMENIMHSQNCEIKELKQSREIVLE
Sbjct  901  CLEEVLQNKDNEFALVKHEKEAVICLQNEKDQKLLEMENIMHSQNCEIKELKQSREIVLE  960

Query  963  DLKKLHVENDEKLQLLRAELQSLEQSHLKELEDTLQVRHIQEFEKVMTDHRVSLEELKKE  1022
            DLKKLHVENDEKLQLLRAELQSLEQSHLKELEDTLQVRHIQEFEKVMTDHRVSLEELKKE
Sbjct  961  DLKKLHVENDEKLQLLRAELQSLEQSHLKELEDTLQVRHIQEFEKVMTDHRVSLEELKKE  1020

Query  1023 NQQIINQIQESHAEIIQEKEKQLQELKLKVSDLSDTRCKLEVELALKEAETDEIKILLEE  1082
            NQQIINQIQESHAEIIQEKEKQLQELKLKVSDLSDTRCKLEVELALKEAETDEIKILLEE
Sbjct  1021 NQQIINQIQESHAEIIQEKEKQLQELKLKVSDLSDTRCKLEVELALKEAETDEIKILLEE  1080

Query  1083 SRAQQKETLKSLLEQETENLRTEISKLNQKIQDNNENYQVGLAELRTLMTIEKDQCISEL  1142
            SRAQQKETLKSLLEQETENLRTEISKLNQKIQDNNENYQVGLAELRTLMTIEKDQCISEL
Sbjct  1081 SRAQQKETLKSLLEQETENLRTEISKLNQKIQDNNENYQVGLAELRTLMTIEKDQCISEL  1140

Query  1143 ISRHEEESNILKAELNKVTSLHNQAFEIEKNLKEQIIELQSKLDSELSALERQKDEKITQ  1202
            ISRHEEESNILKAELNKVTSLHNQAFEIEKNLKEQIIELQSKLDSELSALERQKDEKITQ
Sbjct  1141 ISRHEEESNILKAELNKVTSLHNQAFEIEKNLKEQIIELQSKLDSELSALERQKDEKITQ  1200

Query  1203 QEEKYEAIIQNLEKDRQKLVSSQEQDREQLIQKLNCEKDEAIQTALKEFKLEREVVEKEL  1262
            QEEKYEAIIQNLEKDRQKLVSSQEQDREQLIQKLNCEKDEAIQTALKEFKLEREVVEKEL
Sbjct  1201 QEEKYEAIIQNLEKDRQKLVSSQEQDREQLIQKLNCEKDEAIQTALKEFKLEREVVEKEL  1260

Query  1263 LEKVKHLENQIAKSPAIDSTRGDSSSLVAELQEKLQEEKAKFLEQLEEQEKRKNEEMQNV  1322
            LEKVKHLENQIAKSPAIDSTRGDSSSLVAELQEKLQEEKAKFLEQLEEQEKRKNEEMQNV
Sbjct  1261 LEKVKHLENQIAKSPAIDSTRGDSSSLVAELQEKLQEEKAKFLEQLEEQEKRKNEEMQNV  1320

Query  1323 RTSLIAEQQTNFNTVLTREKMRKENIINDLSDKLKSTMQQQERDKDLIESLSEDRARLLE  1382
            RTSLIAEQQTNFNTVLTREKMRKENIINDLSDKLKSTMQQQERDKDLIESLSEDRARLLE
Sbjct  1321 RTSLIAEQQTNFNTVLTREKMRKENIINDLSDKLKSTMQQQERDKDLIESLSEDRARLLE  1380

Query  1383 EKKKLEEEVSKLRSSSFVPSPYVATAPELYGACAPELPGESDRSAVETADEGRVDSAMET  1442
            EKKKLEEEVSKLRSSSFVPSPYVATAPELYGACAPELPGESDRSAVETADEGRVDSAMET
Sbjct  1381 EKKKLEEEVSKLRSSSFVPSPYVATAPELYGACAPELPGESDRSAVETADEGRVDSAMET  1440

Query  1443 SMMSVQENIHMLSEEKQRIMLLERTLQLKEEENKRLNQRLMSQSMSSVSSRHSEKIAIRD  1502
            SMMSVQENIHMLSEEKQRIMLLERTLQLKEEENKRLNQRLMSQSMSSVSSRHSEKIAIRD
Sbjct  1441 SMMSVQENIHMLSEEKQRIMLLERTLQLKEEENKRLNQRLMSQSMSSVSSRHSEKIAIRD  1500

Query  1503 FQVGDLVLIILDERHDNYVLFTVSPTLYFLHSESLPALDLKPASGASRRPWVLGKVMEKE  1562
            FQVGDLVLIILDERHDNYVLFTVSPTLYFLHSESLPALDLKPASGASRRPWVLGKVMEKE
Sbjct  1501 FQVGDLVLIILDERHDNYVLFTVSPTLYFLHSESLPALDLKPASGASRRPWVLGKVMEKE  1560
```

```
Query  1563  YCQAKKAQNRFKVPLGTKFYRVKAVSWNKKV  1593
             YCQAKKAQNRFKVPLGTKFYRVKAVSWNKKV
Sbjct  1561  YCQAKKAQNRFKVPLGTKFYRVKAVSWNKKV  1591

CPU time:     0.04 user secs.          0.03 sys. secs     0.07 total secs.
```